

ABSTRACT

Methods and software for associating mobility probes with target macromolecules are discussed. By encoding the identities of macromolecules of interest with a universal set of tag portions complementary to a universal set of mobility probes, reactions varying in their input starting material may be identified using the same universal set of mobility probes. This allows the universal collection of mobility probes to be used in a target macromolecule-independent manner. Software is used to decode the associations between the mobility probes and a given target macromolecular identity.